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Patterns of thousand-seed weight inheritance inF$_1$andF$_2$pea hybrids

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Abstract. **The research aim** is to study the inheritance of a thousand-seed weight trait by F$_1$ and F$_2$ hybrids peas. **Research methods.** The study was conducted at the Chishminskiy plant breeding center of the Bashkir Research Institute – the Subdivision of the Russian Science Academy, located in the Cis-Ural steppe zone, in 2017–2019. The paper describes hybridization with two parental pairs, reciprocal crosses, and resulting pea hybrids. Five varieties were analyzed: Shikhan, Chishminskiy 75, Chishminskiy 80, Chishminskiy 95, Melkosemyannyy 2. The resulting seeds were divided into groups: large, medium-large, medium, medium-small, small. The standard deviation (σ), the coefficient of variation (V$_c$, %), heritability estimate (H^2), and the degree of dominance (h$_p$) were determined. Statistical data were analyzed in Microsoft Office Excel 2010 using Statistica 7.0. **Results.** As a result of the conducted experiments, F$_1$ hybrid peas showed lower thousand-seed weight than the large-seeded parent plants. Whereupon, the large-seeded genotype of a mother plant had a greater effect on the manifestation of this trait in hybrids. F$_2$ hybrid peas expressed a thousand-seed weight trait in an intermediate fashion. However, the average values of this trait were much lower than in F$_1$ hybrids. The coefficient of variation V$_c$ in F$_2$ plants was 24.3–33.3%, the degree of dominance h$_p$ was 0.20–0.32 (incomplete dominance of the trait). **Scientific novelty.** The inheritance of a thousand-seed weight in regional varieties that distinctly differ on this trait and in hybrids obtained by crossing was studied for the first time in conditions of the Republic of Bashkortostan. New large-seeded and small-seeded sources for pea breeding were identified.

Keywords: peas, breeding, crossing, hybrid, thousand-seed weight, seed size, heritability estimate, degree of dominance.

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Introduction

The selection of new varieties is of primary importance in ensuring increased productivity of pea grains [1, p. 604], [2, p. 21]. Currently, intervarietal hybridization plays the most important role among other plant breeding methods as remote hybridization, physical and chemical mutagenesis, experimental polyploidy, and the use of cell, tissue, and organ cultures [3, p. 145].

However, it has some limitations in creating high yielding, readily producible varieties adaptive to local conditions. The way hybrids inherit quantitative traits, and the degree parent genotypes influence their manifestation, are not well understood [4, pp. 21–22]; [5, p. 947], [6, p. 208]. This paper presents the results of research on specific aspects of this problem.

The target is to study the inheritance of a seed size trait (thousand-seed weight) in pea hybrids, and the degree parent plants affect its expression.

Methods

The experiments were conducted at the Chishminskiy plant breeding center of the Bashkir Research Institute – the Subdivision of the Russian Academy of Sciences, in 2017–2019.

Five pea varieties (Shikhan, Chishminskiy 75, Chishminskiy 80, Chishminskiy 95, Melkosemyannyy 2) were used as a material to analyze the way a seed size trait is inherited.

Plant crossing was performed according to the scheme: Shikhan × Melkosemyannyy 2, Chishminskiy 75 × Melkosemyannyy 2, Chishminskiy 80 × Melkosemyannyy 2, Chishminskiy 95 × Melkosemyannyy 2. Backcrossings were carried out as well.

First- and second-generation hybrids were sown using an SKS-6-10 seeder. The predecessor is winter rye. Farming methods are generally accepted for the zone. The area of plant alimentation is 20 × 5 cm. The plot size was determined by the seed presence. Hybrids were planted next to their parent forms.

The inheritance of the seed size trait was studied on F$_1$ and F$_2$ hybrids. Bundles of hybrid swarms were selected for analysis. Seeds were weighed on laboratory scales. As a result of weighting, seeds were divided into groups according to their sizes, shown in table 1.

The analysis involved finding standard deviation (σ), the coefficient of variation (V_c, %), heritability estimate (H^2), and the degree of dominance (h_p). Statistical processing of data resulted from field experiments was conducted following the generally accepted method of B. A. Dospekhov. It was done with the Statistica 10.0 and Microsoft Office Excel 2010 software packages. Each indicator was handled in terms of the mean value (*M*), standard error (±SEM), and confidence interval ($t_{0.05}$ × SEM).

Results

Little is understood on the inheritance of a thousand-seed weight trait, although some studies are devoted to this problem. In 1912, while crossing small-seeded pea samples with large-seeded ones, Tschermak found an intermediate character of a thousand-seed weight inheritance in F_1 and a large variety in size in F_2. The ratio of small seeds to all other transitional types was 1:264, close to the 1:255 tetrahybrid segregation model. Based on this, the Austrian scientist concluded that the small-seeded parent form used in crosses had four recessive genes responsible for the formation of small seeds, the large-seeded parent form had four dominant genes, and the intermediate forms are the result of a combination of recessive and dominant genes [7, p.18], [8, pp. 401–402], [9, p. 64]. Subsequently, Wellensiek used Sg_1, Sg_2, Sg_3, Sg_4 symbols in 1925, and Yarnell applied S_1, S_2, S_3, S_4 signs in 1964 [7, p. 19], [10, p. 15], [11, p. 23].

In 1969–1970 V. H. Khangildin and V. V. Khangildin, using the Sewall Wright formula, calculated the smallest possible number of non-allelic genes responsible for varietal differences in seed size. Dispersion analysis of the thousand-seed weight in varieties with different seed sizes and their hybrids showed that large-seeded varieties differ from Melkosemyannyy 2 variety in the presence of two dominant gene alleles [7, p. 19; 11, p.23]. Melkosemyannyy 2 variety (thousand-seed weight is 80–110 g) has five recessive seed size genes. Large-seeded pea varieties have 4–5 dominant genes involved in the formation of high weight of 1000 seeds. Seed size is mostly determined by the internal genetic potential of the variety and the conditions of its cultivation [12, p. 63], [13, p. 7], [14, pp. 71–72].

The literature indicates that first-generation hybrids are characterized by an intermediate manifestation of the trait with a bias towards the parent form with larger seeds when crossing samples that distinctly differ in a thousand-seed weight. In the second filial generation, there is trait segregation with a predominance of plants with intermediate values of a thousand-seed weight [15, pp. 36–37], [16, p.607].

In our experiments, F_1 hybrids from direct and reverse (reciprocal) crossing being significantly different in the thousand-seed weight were characterized by intermediate values of this trait with a bias towards the large-seeded parent form. However, their thousand-seed weight was lower. Thus, hybrids from large-seeded varieties of mother plants had lower the thousand-seed weight by an average of 15.4%. Hybrid offspring from large-seeded varieties of father plants were 19.8% inferior to them (table 2).

As the experiment results show, the manifestation of the thousand-seed weight trait in F_1 pea hybrids is mostly influenced by the genotype of a large-seeded variety, regardless of whether it is used as a mother or father form. However, it should be noted that in our studies, the manifestation of this trait in pea hybrids was greater when a large-seeded variety was of a mother form.

In our studies, F_2 hybrid offspring were characterized by lower average weight values of 1000 seeds than F_1 hybrid offspring (table 3).

Thus, the obtained data are consistent with the opinion of other researchers regarding the intermediate inheritance of the studied trait in hybrids (fig. 1).

In our experiments, the coefficient of variation in the parent varieties ranged from 6.5 to 12.3%. In the hybrid combinations of the second generation, this indicator varied in the range of 24.3–33.3%. A sharp increase in the coefficient of variation in F_2 hybrids indicates that in addition to environmental factors, there is genotypic segregation making hereditary variability 87–95%. The dominance degree h_p = 0.20–0.32 demonstrates incomplete dominance of the thousand-seed weight trait.

Table 1

Classification of pea seeds by their size

Seed size class	*Weight of 1 seed, g*	*Weight of 1000 seeds, g*
I. Large	*0.280–0.300*	*280–300*
II. Semi-large	*0.250–0.279*	*250–279*
III. Medium	*0.160–0.249*	*160–249*
IV. Semi-small	*0.130–0.159*	*130–159*
V. Small	*0.090–0.129*	*90–129*

Table 2

Thousand-seed weight in F_1 pea hybrids and their parents (2017)

Number of hybrids, pcs	*Weight of 1000 seeds, g*			*Deviation of the weight of 1000 seeds in a hybrid relative to the best parent*	
	Mother plant	*F_1 hybrid*	*Father plant*	*Absolute value, ± g*	*Relative value, ± %*
Direct crosses					
4	*253 ± 5.0*	*214 ± 3.8*	*105 ± 2.8*	*–39*	*–15.4*
Reciprocal crosses					
4	*105 ± 2.3*	*203 ± 3.5*	*253 ± 5.0*	*–50*	*–19.8*

Table 3

Thousand-seed frequency distribution F_2 pea hybrids and their parents (2018)

Varieties and hybrids	*Number of seeds assigned to the size class, pcs*					*Weight of 1000 seeds, g*
	I	*II*	*III*	*IV*	*V*	
Direct crosses						
Shikhan	*352*	*605*	*43*	*0*	*0*	*270 ± 14.6*
Shikhan × Melkosemyannyy 2	*67*	*256*	*370*	*243*	*64*	*206 ± 7.8*
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Chishminskiy 75	*0*	*89*	*859*	*52*	*0*	*220 ± 9.0*
Chishminskiy 75 × Melkosemyannyy 2	*0*	*8*	*240*	*504*	*248*	*180 ± 3.8*
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Chishminskiy 80	*105*	*599*	*296*	*0*	*0*	*256 ± 10.0*
Chishminskiy 80 × Melkosemyannyy 2	*57*	*260*	*470*	*182*	*31*	*206 ± 7.8*
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Chishminskiy 95	*250*	*602*	*148*	*0*	*0*	*263 ± 10.0*
Chishminskiy 95 × Melkosemyannyy 2	*63*	*250*	*375*	*250*	*62*	*206 ± 8.0*
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Reciprocal crosses						
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Melkosemyannyy× Shikhan	*60*	*260*	*373*	*233*	*74*	*201 ± 9.4*
Shikhan	*352*	*605*	*43*	*0*	*0*	*270 ± 14.6*
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Melkosemyannyy 2 × Chishminskiy 75	*0*	*13*	*234*	*491*	*262*	*173 ± 7.8*
Chishminskiy 75	*0*	*89*	*859*	*52*	*0*	*220 ± 9.0*
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Melkosemyannyy 2 × Chishminskiy 80	*70*	*245*	*459*	*192*	*34*	*211 ± 9.0*
Chishminskiy 80	*105*	*599*	*296*	*0*	*0*	*256 ± 10.0*
Melkosemyannyy 2	*0*	*0*	*9*	*840*	*151*	*110 ± 8.6*
Melkosemyannyy 2 × Chishminskiy 95	*72*	*266*	*361*	*255*	*46*	*217 ± 9.8*
Chishminskiy 95	*250*	*602*	*148*	*0*	*0*	*263 ± 10.0*

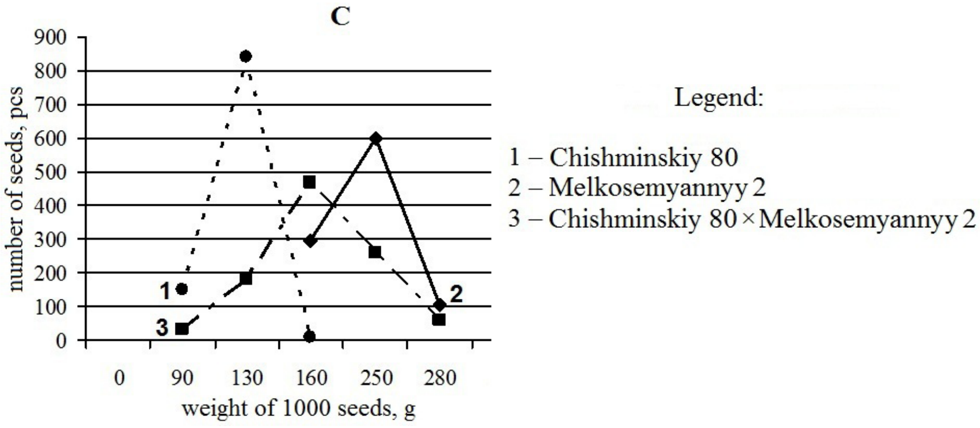

Fig. 1. Seed size frequency distribution in F_2 pea hybrids and their parents

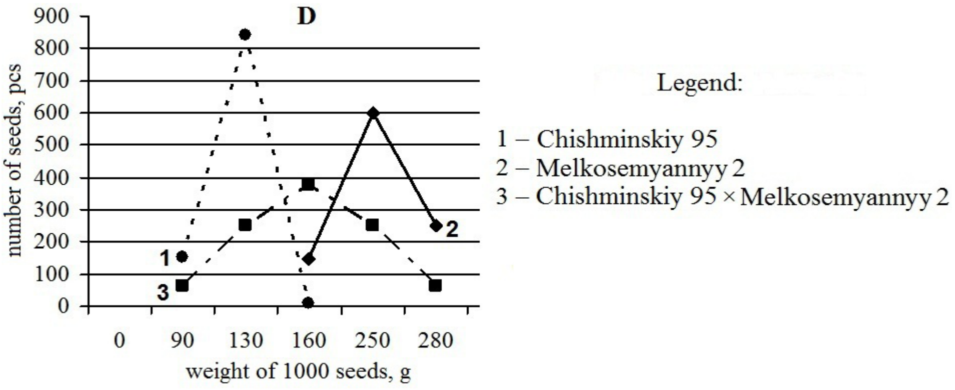

Fig. 2. Pea seeds of different sizes

On the whole, the conducted study showed that crossing local medium- and large-seeded pea varieties Shikhan, Chishminskiy 75, Chishminskiy 80, Chishminskiy 95 with a contrasting small-seeded Melkosemyannyy 2 resulted in intermediate inheritance of the studied trait in the first generation of hybrids.

In the second generation, the trait was split, and the proportion of small-seeded hybrids with 4-5 recessive genes in their genotype ranged from 3.1 to 6.4%. However, there were identified valuable small-seeded F_2 hybrids. The analysis of the hybrid population from a direct crossing of the medium-seeded Chishminskiy 75 and Melkosemyannyy 2 varieties resulted in 8 medium-large, 240 medium, 504 medium-small, 248 small-seeded samples (fig. 2). Moreover, small-seeded and medium-small-seeded hybrids being of interest for breeding purposes were found with a frequency of 24.8 and 50.4%, respectively.

Reciprocal F_2 hybrids by seed size (weight of 1000 seeds) occupied an intermediate position between parent plants with a bias towards the best variety and slightly differed from F_2 hybrids of the direct crossing.

Studying regularities in the inheritance of quantitative traits involved in the formation of pea productivity will improve the efficiency of selection in segregated hybrid swarms. This knowledge is essential when planning crossings, selection of parent pairs, the choice of the breeding methodology. The seed size trait, developed by polymeric genes, can vary greatly depending on the growing conditions. The given study showed that the calculation of the heritability coefficients and variability makes it possible to predict the manifestation of the desired genotypes when crossing varieties characterized by different seed sizes. It resulted in new large- and small-seeded sources for pea breeding, which are being evaluated in the breeding nursery.

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